Cancel Claim 53.

58. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions where a target nucleic acid of 14 nucleotides in length must have no less than 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32;

b) separating unbound target nucleic acids/label from said collection of probe nucleic acid features; and

(c) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features;

wherein said method is further characterized by including a target nucleic acid labeling step prior to said detecting step(c).

59. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions where a target nucleic acid of 14 nucleotides in length must have no less than 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that is chosen from: (i) a probe nucleic acid that forms a stable intramolecular structure; (ii) a probe nucleic acid that comprises reverse polarity nucleotide analogs; and (iii) a probe nucleic acid that comprises abasic phosphodiesters;

(b) separating unbound target nucleic acids/label from said collection of probe nucleic acid features; and

(c) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features;

wherein said method is further characterized by including a target nucleic acid

labeling step prior to said detecting step(c).

60. (Amended) A hybridization assay comprising:

(a) contacting a sample of detectably labeled target nucleic acids under hybridization conditions where a target nucleic acid of 14 nucleotides in length ~~to~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature that is an empirically observed inactive probe that does not hybridize to a fully complementary fluorescently labeled target nucleic acid as determined in an assay wherein said probe is provided in an array that is contacted with said fluorescently labeled fully complementary target under said hybridization conditions;

(b) separating non-hybridized target nucleic acids/label from said array; and

(c) detecting the presence of target nucleic acids hybridized to said array probe nucleic acid features;

wherein said method is further characterized by including a target nucleic acid labeling step prior to said detecting step(c).

64. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions where a target nucleic acid of 14 nucleotides in length must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature that is an empirically observed inactive probe that does not hybridize to its fully complementary target nucleic acid as determined in an assay wherein said probe is provided in an array that is contacted with said fluorescently labeled fully complementary target under said hybridization conditions;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features;

(d) separating unbound label from said array; and

(e) detecting the presence of target nucleic acids hybridized to said array

of probe nucleic acid features.

66. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions where a target nucleic acid of 14 nucleotides in length must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features;

(d) separating unbound label from said array; and

(e) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

67. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions where a target nucleic acid of 14 nucleotides in length must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that is chosen from: (i) a probe nucleic acid that forms a stable intramolecular structure; (ii) a probe nucleic acid that comprises reverse polarity nucleotide analogs; and (iii) a probe nucleic acid that comprises abasic phosphodiesters;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features;

(d) separating unbound label from said array; and

(e) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

71. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions where a target nucleic acid of 14 nucleotides in length must have no less than 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature made up of background probes that do not selectively bind to any of said target nucleic acids;

(b) washing said contacted array to remove unbound target nucleic acids/label from said array; and

(c) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features;

wherein said method is further characterized by including a target nucleic acid labeling step prior to said detecting step(c).

Cancel Claim 74.

REMARKS

In view of the above amendments and the following remarks, the Examiner is respectfully requested to withdraw all of the remaining rejections and allow Claims 50-52; 54-68 and 71-73 and 75-84, the only claims pending and currently under examination in this application following entry of the above amendments.

Amendments

Claims 50, 58, 59, 60 and 71 have been amended to specify that the claim includes both a labeling step and an unbound target nucleic acid/label separation step prior to the detecting step, support for these amendments being found in the previously pending claims and working exemplification, as well as specification, of the present application. Claims 64, 66 and 67 have been amended to include an unbound label separation step prior to the claimed detection step, support for these amendments being found in the previously pending claims and working exemplification, as well as specification, of the present application. Finally, Claims 50, 60 and 64 have been amended to clarify that the background probes do not